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Ala Lys Asp Ala Gly Tyr Arg Lys Pro Leu Arg Glu Phe Gln Leu Arg
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Ala Glu Asp Pro Lys Pro Ile Ile Lys Glu Arg Val His Phe Phe Ala
225             230             235             240

Glu Thr Gly Ile Thr Phe Arg Pro Asp Val Phe Lys Thr Arg Ser Val
            245             250             255

Val Pro Ala Glu Glu Pro Val Glu Gln Arg Thr Glu Phe Lys Val Ser
            260             265             270

Gln Met Leu Asp Trp Leu Leu Gln Leu Asp Asn Asn Thr Trp Gln Pro
        275             280             285

His Leu Lys Leu Phe Ser Arg Ile Gln Leu Gly Leu Ser Lys Thr Tyr
    290             295             300

Ala Ile Met Thr Leu Glu Pro His Gln Ile Arg His His Lys Thr Asp
305             310             315             320

Leu Leu Ser Pro Ser Gly Thr Gly Glu Val Met Asn Asp Gly Val Gly
            325             330             335

Arg Met Ser Arg Ser Val Ala Lys Arg Ile Arg Asp Val Leu Gly Leu
```

                    340                    345                    350

Gly Asp Val Pro Ser Ala Val Gln Gly Arg Phe Gly Ser Ala Lys Gly
        355             360             365

Met Trp Val Ile Asp Val Asp Asp Thr Gly Asp Glu Asp Trp Ile Glu
    370             375             380

Thr Tyr Pro Ser Gln Arg Lys Trp Glu Cys Asp Phe Val Asp Lys His
385             390             395             400

Gln Arg Thr Leu Glu Val Arg Ser Val Ala Ser Glu Leu Lys Ser Ala
            405             410             415

Gly Leu Asn Leu Gln Leu Leu Pro Val Leu Glu Asp Arg Ala Arg Asp
        420             425             430

Lys Val Lys Met Arg Gln Ala Ile Gly Asp Arg Leu Ile Asn Asp Leu
    435             440             445

Gln Arg Gln Phe Ser Glu Gln Lys His Ala Leu Asn Arg Pro Val Glu
    450             455             460

Phe Arg Gln Trp Val Tyr Glu Ser Tyr Ser Ser Arg Ala Thr Arg Val
465             470             475             480

Ser His Gly Arg Val Pro Phe Leu Ala Gly Leu Pro Asp Ser Gln Glu
            485             490             495

Glu Thr Leu Asn Phe Leu Met Asn Ser Gly Phe Asp Pro Lys Lys Gln
        500             505             510

Lys Tyr Leu Gln Asp Ile Ala Trp Asp Leu Gln Lys Arg Lys Cys Asp
        515             520             525

Thr Leu Lys Ser Lys Leu Asn Ile Arg Val Gly Arg Ser Ala Tyr Ile
    530             535             540

Tyr Met Ile Ala Asp Phe Trp Gly Val Leu Glu Glu Asn Glu Val His
545             550             555             560

Val Gly Phe Ser Ser Lys Phe Arg Asp Glu Glu Glu Ser Phe Thr Leu
            565             570             575

Leu Ser Asp Cys Asp Val Leu Val Ala Arg Ser Pro Ala His Phe Pro
        580             585             590

```
Ser Asp Ile Gln Arg Val Arg Ala Val Phe Lys Pro Glu Leu His Ser
        595             600         605

Leu Lys Asp Val Ile Ile Phe Ser Thr Lys Gly Asp Val Pro Leu Ala
        610             615             620

Lys Lys Leu Ser Gly Gly Asp Tyr Asp Gly Asp Met Ala Trp Val Cys
625             630             635                         640

Trp Asp Pro Glu Ile Val Asp Gly Phe Val Asn Ala Glu Met Pro Leu
                645             650                 655

Glu Pro Asp Leu Ser Arg Tyr Leu Lys Lys Asp Lys Thr Thr Phe Lys
            660             665             670

Gln Leu Met Ala Ser His Gly Thr Gly Ser Ala Ala Lys Glu Gln Thr
        675             680             685

Thr Tyr Asp Met Ile Gln Lys Ser Phe His Phe Ala Leu Gln Pro Asn
    690             695             700

Phe Leu Gly Met Cys Thr Asn Tyr Lys Glu Arg Leu Cys Tyr Ile Asn
705             710             715                         720

Asn Ser Val Ser Asn Lys Pro Ala Ile Ile Leu Ser Ser Leu Val Gly
                725             730             735

Asn Leu Val Asp Gln Ser Lys Gln Gly Ile Val Phe Asn Glu Ala Ser
            740             745             750

Trp Ala Gln Leu Arg Arg Glu Leu Leu Gly Gly Ala Leu Ser Leu Pro
        755             760             765

Asp Pro Met Tyr Lys Ser Asp Ser Trp Leu Gly Arg Gly Glu Pro Thr
    770             775             780

His Ile Ile Asp Tyr Leu Lys Phe Ser Ile Ala Arg Pro Ala Ile Asp
785             790             795                         800

Lys Glu Leu Glu Ala Phe His Asn Ala Met Lys Ala Ala Lys Asp Thr
            805             810             815

Glu Asp Gly Ala His Phe Trp Asp Pro Asp Leu Ala Ser Tyr Tyr Thr
        820             825             830
```

Phe Phe Lys Glu Ile Ser Asp Lys Ser Arg Ser Ser Ala Leu Leu Phe
     835                840              845

Thr Thr Leu Lys Asn Arg Ile Gly Glu Val Glu Lys Glu Tyr Gly Arg
     850                855              860

Leu Val Lys Asn Lys Glu Met Arg Asp Ser Lys Asp Pro Tyr Pro Val
865                870          875              880

Arg Val Asn Gln Val Tyr Glu Lys Trp Cys Ala Ile Thr Pro Glu Ala
          885            890            895

Met Asp Lys Ser Gly Ala Asn Tyr Asp Ser Lys Val Ile Arg Leu Leu
        900            905            910

Glu Leu Ser Phe Leu Ala Asp Arg Glu Met Asn Thr Trp Ala Leu Leu
     915              920           925

Arg Ala Ser Thr Ala Phe Lys Leu Tyr Tyr His Lys Ser Pro Lys Phe
     930             935          940

Val Trp Gln Met Ala Gly Arg Gln Leu Ala Tyr Ile Lys Ala Gln Met
945              950          955            960

Thr Ser Arg Pro Gly Glu Gly Ala Pro Ala Leu Met Thr Ala Phe Met
        965            970            975

Tyr Ala Gly Leu Met Pro Asp Lys Lys Phe Thr Lys Gln Tyr Val Ala
        980            985          990

Arg Leu Glu Gly Asp Gly Ser Glu Tyr Pro Asp Pro Glu Val Tyr Glu
     995             1000          1005

Val Leu Gly Asp Asp Asp Phe Asp Gly Ile Gly Phe Thr Gly Asn
   1010             1015          1020

Gly Asp Tyr
   1025

&lt;210&gt;  5
&lt;211&gt;  30
&lt;212&gt;  DNA
&lt;213&gt;  Artificial Sequence

&lt;220&gt;
&lt;223&gt;  artificial sequence is primer

```
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<210>   6
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   6
ttttctgaat tctcttgccg cttttattct                                    30


<210>   7
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   7
gccaagcttc catgaaccct attactccta                                    30


<210>   8
<211>   28
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   8
ccgaattcat aatcgccatt ccctgtga                                      28


<210>   9
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   9
gctcaaatcc catggctcgg agcgaagaaa                                    30


<210>   10
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   10
```

```
ccgaattcta ataatcgcca ttccctgtga                                          30
```

```
<210>   11
<211>   20
<212>   RNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   11
guuuucacccc uauccucccc                                                    20
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```
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<211>   20
<212>   RNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is primer

<400>   12
cgacucaugg accuugggag                                                     20
```

```
<210>   13
<211>   8
<212>   PRT
<213>   Neurospora crassa

<220>
<221>   MISC_FEATURE
<222>   (1)..(8)
<223>   Xaa is any amino acid

<400>   13

Gly Ser Asp Leu Asp Gly Asp Xaa
1                   5
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```
<210>   14
<211>   129
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   artificial sequence is tag sequence

<400>   14
gaattctgca gatatccagc acagtggcgg ccgctcgagt ctagagggcc cttcgaaggt    60

aagcctatcc ctaaccctct cctcggtctc gattctacgc gtaccggtca tcatcaccat    120

caccattga                                                             129
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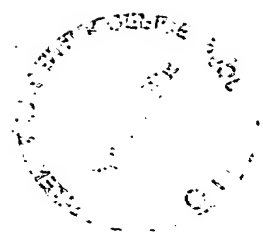
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<210>   15
```

<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial sequence is tag sequence

<400> 15

Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu Ser Arg Gly
1               5               10              15


Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
            20              25              30


Thr Arg Thr Gly His His His His His His
        35              40